

30	35	40	45	
aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa	Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu	195		
50	55	60		
tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct	Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser	243		
65	70	75		
atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac	Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr	291		
80	85	90		
ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg	Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met	339		
95	100	105		
gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc	Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile	387		
110	115	120	125	
tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa	Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys	435		
130	135	140		
tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc	Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe	483		
145	150	155		
gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac	Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn	531		
160	165	170		
ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac	Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His	579		
175	180	185		
gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac	Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His	627		
190	195	200	205	
cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac	Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn	675		
210	215	220		
gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc	Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile	723		
225	230	235		
ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac	Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr	771		
240	245	250		
atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta	Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val	819		
255	260	265		
ggg atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg	Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met	867		
270	275	280	285	

act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc	915
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe	
290 295 300	
atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac	963
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn	
305 310 315	
aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt	1011
Asn Asp Arg Val Tyr Ile Asn Val Val Lys Asn Lys Glu Tyr Arg	
320 325 330	
ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct	1059
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala	
335 340 345	
ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa	1107
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys	
350 355 360 365	
tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag	1155
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln	
370 375 380	
gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac	1203
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn	
385 390 395	
aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa	1251
Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu	
400 405 410	
cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat	1299
Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp	
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gac ggt tgg ggt gaa cgt ccg ctg taa gaattc	1332
Asp Gly Trp Gly Glu Arg Pro Leu *	
430 435	

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<220>

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20 25 30	
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp	
35 40 45	
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys	
50 55 60	
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu	
65 70 75 80	

gaattcga	aaa	cg	atg	tct	acc	ttc	act	gaa	tac	atc	aag	aac	atc	atc	aat	51
			Met	Ser	Thr	Phe	Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	
			1				5					10				
acc	tcc	atc	ctg	aac	ctg	cgc	tac	gaa	tcc	aat	cac	ctg	atc	gac	ctg	99
Thr	Ser	Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	
	15					20					25					
tct	cgc	tac	gct	tcc	aaa	atc	aac	atc	ggt	tct	aaa	ggt	aac	ttc	gat	147
Ser	Arg	Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	
	30				35				40					45		
ccg	atc	gac	aag	aat	cag	atc	cag	ctg	ttc	aat	ctg	gaa	tct	tcc	aaa	195
Pro	Ile	Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	
				50					55					60		
atc	gaa	ggt	atc	ctg	aag	aat	gct	atc	gta	tac	aac	tct	atg	tac	gaa	243
Ile	Glu	Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	
			65				70					75				
aac	ttc	tcc	acc	tcc	ttc	tgg	atc	cgt	atc	ccg	aaa	tac	ttc	aac	tcc	291
Asn	Phe	Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	
		80					85					90				
atc	tct	ctg	aac	aat	gaa	tac	acc	atc	atc	aac	tgc	atg	gaa	aac	aat	339
Ile	Ser	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	
	95				100						105					
tct	ggt	tgg	aaa	gta	tct	ctg	aac	tac	ggt	gaa	atc	atc	tgg	act	ctg	387
Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	
	110				115					120				125		
cag	gac	act	cag	gaa	atc	aaa	cag	cgt	ggt	gta	ttc	aaa	tac	tct	cag	435
Gln	Asp	Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	
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atg	atc	aac	atc	tct	gac	tac	atc	aat	cgc	tgg	atc	ttc	ggt	acc	atc	483
Met	Ile	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	
			145					150					155			
acc	aac	aat	cgt	ctg	aat	aac	tcc	aaa	atc	tac	atc	aac	ggc	cgt	ctg	531
Thr	Asn	Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	
		160					165					170				
atc	gac	cag	aaa	ccg	atc	tcc	aat	ctg	ggt	aac	atc	cac	gct	tct	aat	579
Ile	Asp	Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	
	175					180					185					
aac	atc	atg	ttc	aaa	ctg	gac	ggt	tgt	cgt	gac	act	cac	cgc	tac	atc	627
Asn	Ile	Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	
	190				195					200				205		
tgg	atc	aaa	tac	ttc	aat	ctg	ttc	gac	aaa	gaa	ctg	aac	gaa	aaa	gaa	675
Trp	Ile	Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	
				210					215					220		
atc	aaa	gac	ctg	tac	gac	aac	cag	tcc	aat	tct	ggt	atc	ctg	aaa	gac	723
Ile	Lys	Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	
			225					230					235			
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[illegible]

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<211> 434
<212> PRT
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			20					25					30		
Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp
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Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val
	50					55					60				
Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser
65					70					75					80
Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu
				85					90					95	
Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp
			100					105					110		
Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr
		115					120					125			
Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile	Asn
	130					135					140				
Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn
145					150					155					160
Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp	Gln
				165					170					175	
Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile	Met
			180					185					190		
Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile	Lys
	195						200					205			
Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys	Asp
	210					215					220				
Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp	Gly
225					230					235				240	
Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr	Asp
				245					250					255	
Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr	Met
			260					265					270		
Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr	Leu
	275						280					285			
Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr	Ala
	290					295					300				
Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr	Ile
305					310					315					320
Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala	Ser
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Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp	Val
			340					345					350		
Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln	Gly
	355						360					365			
Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn	Asp
	370					375					380				
Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu	Val
385					390					395					400
Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr	Leu
				405					410					415	
Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp	Gly	Glu	Arg
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Pro	Leu														

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[illegible]

<221> CDS

<400> 5

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 <211> 435
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<400> 6

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			20					25					30		
Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile
			35				40					45			
Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu
			50			55					60				
Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe
65					70					75					80
Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser
				85					90					95	
Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly
			100					105						110	
Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp
			115				120						125		
Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile
			130			135						140			
Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn
145					150					155					160
Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp
				165					170					175	
Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile
			180					185					190		
Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile
		195					200					205			
Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys
		210				215					220				
Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp
225					230					235					240
Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr
				245					250					255	
Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr
			260					265					270		
Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr
		275					280						285		
Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr
		290				295					300				
Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr
305					310					315					320
Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala
				325					330					335	
Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp
			340					345					350		
Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln
		355				360						365			
Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn
		370				375					380				
Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu
385					390					395					400
Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr
				405					410					415	

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130							135							140							
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Asn	Glu	Asp	Ser	Glu	Gln	Ser	Ile	Asn	Phe	Ser	Tyr	Asp	Ile	Ser	Asn						
		145					150					155									
aac	gct	cct	ggt	tac	aac	aag	tgg	ttc	ttc	gtc	acc	gtc	acc	aac	aac	531					
Asn	Ala	Pro	Gly	Tyr	Asn	Lys	Trp	Phe	Phe	Val	Thr	Val	Thr	Asn	Asn						
		160				165					170										
atg	atg	ggt	aac	atg	aag	atc	tac	atc	aac	ggt	aag	ctg	atc	gac	acc	579					
Met	Met	Gly	Asn	Met	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Ile	Asp	Thr						
		175			180					185					190						
atc	aag	gtc	aag	gag	ttg	acc	ggt	atc	aac	ttc	tcc	aag	acc	atc	acc	627					
Ile	Lys	Val	Lys	Glu	Leu	Thr	Gly	Ile	Asn	Phe	Ser	Lys	Thr	Ile	Thr						
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ttc	gag	atc	aac	aag	atc	cca	gac	acc	ggt	ctg	atc	acc	tcc	gac	tcc	675					
Phe	Glu	Ile	Asn	Lys	Ile	Pro	Asp	Thr	Gly	Leu	Ile	Thr	Ser	Asp	Ser						
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gac	aac	atc	aac	atg	tgg	atc	cgt	gac	ttc	tac	atc	ttc	gcc	aag	gag	723					
Asp	Asn	Ile	Asn	Met	Trp	Ile	Arg	Asp	Phe	Tyr	Ile	Phe	Ala	Lys	Glu						
		225					230					235									
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Leu	Asp	Gly	Lys	Asp	Ile	Asn	Ile	Leu	Phe	Asn	Ser	Leu	Gln	Tyr	Thr						
	240					245					250										
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Asn	Val	Val	Lys	Asp	Tyr	Trp	Gly	Asn	Asp	Leu	Arg	Tyr	Asn	Lys	Glu						
	255				260					265					270						
tac	tac	atg	gtc	aac	atc	gac	tac	ttg	aac	aga	tac	atg	tac	gcc	aac	867					
Tyr	Tyr	Met	Val	Asn	Ile	Asp	Tyr	Leu	Asn	Arg	Tyr	Met	Tyr	Ala	Asn						
				275					280					285							
tcc	aga	cag	atc	gtc	ttc	aac	acc	aga	cgt	aac	aac	aac	gac	ttc	aac	915					
Ser	Arg	Gln	Ile	Val	Phe	Asn	Thr	Arg	Arg	Asn	Asn	Asn	Asp	Phe	Asn						
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gag	ggt	tac	aag	atc	atc	atc	aag	cgt	atc	aga	ggt	aac	acc	aac	gac	963					
Glu	Gly	Tyr	Lys	Ile	Ile	Ile	Lys	Arg	Ile	Arg	Gly	Asn	Thr	Asn	Asp						
		305					310					315									
acc	aga	gtc	aga	ggt	ggt	gac	atc	ctg	tac	ttc	gac	atg	act	atc	aac	1011					
Thr	Arg	Val	Arg	Gly	Gly	Asp	Ile	Leu	Tyr	Phe	Asp	Met	Thr	Ile	Asn						
		320				325					330										
aac	aag	gcc	tac	aac	ctg	ttc	atg	aag	aac	gag	acc	atg	tac	gcc	gac	1059					
Asn	Lys	Ala	Tyr	Asn	Leu	Phe	Met	Lys	Asn	Glu	Thr	Met	Tyr	Ala	Asp						
	335				340					345					350						
aac	cac	tcc	acc	gag	gac	atc	tac	gcc	atc	ggt	ctg	cgt	gag	cag	acc	1107					
Asn	His	Ser	Thr	Glu	Asp	Ile	Tyr	Ala	Ile	Gly	Leu	Arg	Glu	Gln	Thr						
				355				360						365							
aag	gac	atc	aac	gac	aac	atc	atc	ttc	cag	atc	cag	cca	atg	aac	aac	1155					
Lys	Asp	Ile	Asn	Asp	Asn	Ile	Ile	Phe	Gln	Ile	Gln	Pro	Met	Asn	Asn						
			370					375					380								

act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag	1203
Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu	
385 390 395	
aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt	1251
Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly	
400 405 410	
ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt	1299
Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly	
415 420 425 430	
aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc	1347
Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val	
435 440 445	
cca gtc tcc gag taataggaat tc	1371
Pro Val Ser Glu	
450	

<210> 10
 <211> 450
 <212> PRT
 <213> Synthetic Construct

<220>

<400> 10																			
Met	Thr	Ile	Pro	Phe	Asn	Ile	Phe	Ser	Tyr	Thr	Asn	Asn	Ser	Leu	Leu				
1				5					10					15					
Lys	Asp	Ile	Ile	Asn	Glu	Tyr	Phe	Asn	Asn	Ile	Asn	Asp	Ser	Lys	Ile				
		20						25					30						
Leu	Ser	Leu	Gln	Asn	Arg	Lys	Asn	Thr	Leu	Val	Asp	Thr	Ser	Gly	Tyr				
		35					40					45							
Asn	Ala	Glu	Val	Ser	Glu	Glu	Gly	Asp	Val	Gln	Leu	Asn	Pro	Ile	Phe				
		50				55					60								
Pro	Phe	Asp	Phe	Lys	Leu	Gly	Ser	Ser	Gly	Glu	Asp	Arg	Gly	Lys	Val				
					70					75				80					
Ile	Val	Thr	Gln	Asn	Glu	Asn	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Ser				
				85					90					95					
Phe	Ser	Ile	Ser	Phe	Trp	Ile	Arg	Ile	Asn	Lys	Trp	Val	Ser	Asn	Leu				
			100					105					110						
Pro	Gly	Tyr	Thr	Ile	Ile	Asp	Ser	Val	Lys	Asn	Asn	Ser	Gly	Trp	Ser				
		115				120						125							
Ile	Gly	Ile	Ile	Ser	Asn	Phe	Leu	Val	Phe	Thr	Leu	Lys	Gln	Asn	Glu				
		130				135					140								
Asp	Ser	Glu	Gln	Ser	Ile	Asn	Phe	Ser	Tyr	Asp	Ile	Ser	Asn	Asn	Ala				
				150					155						160				
Pro	Gly	Tyr	Asn	Lys	Trp	Phe	Phe	Val	Thr	Val	Thr	Asn	Asn	Met	Met				
				165					170					175					
Gly	Asn	Met	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Ile	Asp	Thr	Ile	Lys				
			180					185					190						
Val	Lys	Glu	Leu	Thr	Gly	Ile	Asn	Phe	Ser	Lys	Thr	Ile	Thr	Phe	Glu				
			195				200					205							
Ile	Asn	Lys	Ile	Pro	Asp	Thr	Gly	Leu	Ile	Thr	Ser	Asp	Ser	Asp	Asn				
		210				215					220								
Ile	Asn	Met	Trp	Ile	Arg	Asp	Phe	Tyr	Ile	Phe	Ala	Lys	Glu	Leu	Asp				
					230					235					240				
225																			

Asp	Phe	Lys	Leu	Ser	Ser	Gly	Asp	Lys	Ile	Ile	Val	Asn	Leu	Asn		
80					85					90						
aac	aac	atc	ttg	tac	tcc	gcc	atc	tac	gag	aac	tcc	tct	gtc	tcc	ttc	339
Asn	Asn	Ile	Leu	Tyr	Ser	Ala	Ile	Tyr	Glu	Asn	Ser	Ser	Val	Ser	Phe	
95					100					105					110	
tggt	atc	aag	atc	tcc	aag	gac	ttg	acc	aac	tcc	cac	aac	gag	tac	acc	387
Trp	Ile	Lys	Ile	Ser	Lys	Asp	Leu	Thr	Asn	Ser	His	Asn	Glu	Tyr	Thr	
				115					120					125		
atc	atc	aac	tcc	atc	gag	cag	aac	tcc	gggt	tggt	aag	ttg	tgt	atc	cgt	435
Ile	Ile	Asn	Ser	Ile	Glu	Gln	Asn	Ser	Gly	Trp	Lys	Leu	Cys	Ile	Arg	
			130					135					140			
aac	gggt	aac	atc	gag	tggt	atc	ttg	cag	gac	gtc	aac	cgt	aag	tac	aag	483
Asn	Gly	Asn	Ile	Glu	Trp	Ile	Leu	Gln	Asp	Val	Asn	Arg	Lys	Tyr	Lys	
		145					150					155				
tcc	ttg	atc	ttc	gac	tac	tcc	gag	tcc	ttg	tcc	cac	acc	gggt	tac	acc	531
Ser	Leu	Ile	Phe	Asp	Tyr	Ser	Glu	Ser	Leu	Ser	His	Thr	Gly	Tyr	Thr	
	160					165					170					
aac	aag	tggt	ttc	ttc	gtc	acc	atc	acc	aac	aac	atc	atg	gggt	tac	atg	579
Asn	Lys	Trp	Phe	Phe	Val	Thr	Ile	Thr	Asn	Asn	Ile	Met	Gly	Tyr	Met	
175					180					185					190	
aag	ttg	tac	atc	aac	gggt	gag	ttg	aag	cag	tcc	cag	aag	atc	gag	gac	627
Lys	Leu	Tyr	Ile	Asn	Gly	Glu	Leu	Lys	Gln	Ser	Gln	Lys	Ile	Glu	Asp	
				195					200					205		
ctgt	gac	gag	gtc	aag	ctgt	gac	aag	acc	atc	gtc	ttc	gggt	atc	gac	gag	675
Leu	Asp	Glu	Val	Lys	Leu	Asp	Lys	Thr	Ile	Val	Phe	Gly	Ile	Asp	Glu	
			210					215					220			
aac	atc	gac	gag	aac	cag	atg	ttg	tggt	att	cgt	gac	ttc	aac	atc	ttc	723
Asn	Ile	Asp	Glu	Asn	Gln	Met	Leu	Trp	Ile	Arg	Asp	Phe	Asn	Ile	Phe	
		225				230						235				
tcc	aag	gag	ctgt	tcc	aac	gag	gac	atc	aac	atc	gtc	tac	gag	gggt	cag	771
Ser	Lys	Glu	Leu	Ser	Asn	Glu	Asp	Ile	Asn	Ile	Val	Tyr	Glu	Gly	Gln	
	240					245					250					
atc	ctgt	agg	aac	gtc	atc	aag	gac	tac	tggt	gggt	aac	cca	ctgt	aag	ttc	819
Ile	Leu	Arg	Asn	Val	Ile	Lys	Asp	Tyr	Trp	Gly	Asn	Pro	Leu	Lys	Phe	
255					260					265					270	
gac	acc	gag	tac	tac	atc	atc	aac	gac	aac	tac	atc	gac	cgt	tac	atc	867
Asp	Thr	Glu	Tyr	Tyr	Ile	Ile	Asn	Asp	Asn	Tyr	Ile	Asp	Arg	Tyr	Ile	
				275					280					285		
gcc	cca	gag	tcc	aac	gtc	ctgt	gtc	ctgt	gtc	cag	tac	cct	gac	ctgt	tcc	915
Ala	Pro	Glu	Ser	Asn	Val	Leu	Val	Leu	Val	Gln	Tyr					

320	325	330	
ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile 335 340 345 350			1059
tac gcc acc cag ggt ggt gag tgt tcc cag aac tgt gtc tac gcc ctg Tyr Ala Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu 355 360 365			1107
aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile 370 375 380			1155
aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser 385 390 395			1203
ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg 400 405 410			1251
ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu 415 420 425 430			1299
acc aag ctg ctg tcc acc tcc tcc ttc tgg aag ttc atc tcc cgt gac Thr Lys Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp 435 440 445			1347
cca ggt tgg gtc gag taataggaat tc Pro Gly Trp Val Glu 450			1374

<210> 12
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12
 Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
 1 5 10 15
 Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
 20 25 30
 Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
 35 40 45
 Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
 50 55 60
 Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
 65 70 75 80
 Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
 85 90 95
 Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
 100 105 110
 Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
 115 120 125
 Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly

<220>

<223> Synthetic Construct

<221> CDS

<222> (10)...(1305)

<400> 15

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gaattcacg atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51
      Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
        1             5             10

aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac 99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
  15             20             25             30

gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc 147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
          35             40             45

atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga 195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
          50             55             60

atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac 243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
          65             70             75

atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc 291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
      80             85             90

cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc 339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
  95             100             105             110

atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg 387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
          115             120             125

aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat 435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
          130             135             140

cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac 483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
          145             150             155

atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac 531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
          160             165             170

tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc 579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
          175             180             185             190

aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc 627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
          195             200             205

ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc 675
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Gly	Cys	Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	
			210					215					220			
gac	act	gag	ttg	ggt	aag	acc	gag	atc	gag	acc	ttg	tac	tcc	gac	gag	723
Asp	Thr	Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	
		225					230					235				
cct	gac	cca	tcc	atc	ctg	aag	gac	ttc	tgg	ggt	aac	tac	ctg	ctg	tac	771
Pro	Asp	Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	
		240				245					250					
aac	aaa	cgt	tac	tac	ttg	ctg	aac	ttg	ttg	cgt	acc	gac	aag	tcc	atc	819
Asn	Lys	Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	
255					260					265					270	
acc	cag	aac	tcc	aac	ttc	ttg	aac	atc	aac	cag	cag	aga	ggt	gtc	tac	867
Thr	Gln	Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	
				275					280					285		
cag	aag	cca	aac	atc	ttc	tcc	aac	acc	aga	ttg	tac	acc	gga	gtc	gag	915
Gln	Lys	Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	
			290					295					300			
gtc	att	atc	aga	aag	aac	gga	tct	act	gat	att	tcc	aac	acc	gat	aac	963
Val	Ile	Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	
		305				310						315				
ttc	gtc	aga	aag	aac	gat	ctg	gct	tac	atc	aac	ggt	gtc	gac	aga	gat	1011
Phe	Val	Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	
			320			325					330					
gtc	gaa	tac	cgt	ctg	tac	gcc	gat	atc	tct	atc	gcc	aaa	cct	gaa	aag	1059
Val	Glu	Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	
335					340					345				350		
atc	atc	aag	ctg	atc	cgt	acc	tct	aac	tct	aac	aac	tct	ctg	gga	caa	1107
Ile	Ile	Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	
				355				360					365			
atc	atc	gtc	atg	gac	tcc	atc	ggt	aat	aac	tgt	acc	atg	aac	ttc	cag	1155
Ile	Ile	Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	
			370				375					380				
aac	aac	aac	ggt	gga	aac	atc	ggt	ttg	ttg	ggt	ttc	cac	tcc	aac	aac	1203
Asn	Asn	Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	
		385				390					395					
ttg	gtc	gct	tcc	tcc	tgg	tac	tac	aac	aac	atc	cgt	aag	aac	acc	tcc	1251
Leu	Val	Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser	
		400				405					410					
tcc	aac	ggt	tgc	ttc	tgg	tcc	ttc	atc	tcc	aag	gag	cac	ggt	tgg	cag	1299
Ser	Asn	Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His				

<210> 16

<211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16
 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
 1 5 10 15
 Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
 20 25 30
 Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
 35 40 45
 Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
 50 55 60
 Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
 65 70 75 80
 Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
 85 90 95
 Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
 100 105 110
 Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
 115 120 125
 Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
 130 135 140
 Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
 145 150 155 160
 Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
 165 170 175
 Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
 180 185 190
 Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
 195 200 205
 Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
 210 215 220
 Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
 225 230 235 240
 Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
 245 250 255
 Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
 260 265 270
 Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
 275 280 285
 Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
 290 295 300
 Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
 305 310 315 320
 Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
 325 330 335
 Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
 340 345 350
 Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
 355 360 365
 Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
 370 375 380
 Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
 385 390 395 400
 Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
 405 410 415
 Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn

420

425

430

<210> 17
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (10)...(1356)

<400> 17

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gaattcacg atg aag gac acc atc ctg atc cag gtc ttc aac aac tac atc 51
      Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile
        1             5             10

tcc aac atc tcc tcc aac gcc atc ctg tcc ctg tcc tac cgt ggt ggt 99
Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly
  15             20             25             30

cgt ctg atc gac tcc tcc ggt tac gga gcc acc atg aac gtc ggt tcc 147
Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser
          35             40             45

gac gtc atc ttc aac gac atc ggt aac ggt cag ttc aag ctg aac aac 195
Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn
          50             55             60

tcc gag aac tcc aac atc acc gcc cac cag tcc aag ttc gtc gtc tac 243
Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr
          65             70             75

gac tcc atg ttc gac aac ttc tcc atc aac ttc tgg gtc cgt acc cca 291
Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro
          80             85             90

aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc 339
Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr
          95             100            105            110

atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag 387
Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys
          115            120            125

gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag 435
Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys
          130            135            140

tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc 483
Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile
          145            150            155

aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc 531
Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala
          160            165            170

aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac 579
Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn

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aag ctg cgt ctg gga tgt aac tgg cag ttc atc cca gtc gac gag ggt 1347
 Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly
 435 440 445

tgg acc gag taataggaat tc 1368
 Trp Thr Glu

<210> 18
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18
 Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
 1 5 10 15
 Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
 20 25 30
 Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
 35 40 45
 Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
 50 55 60
 Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser
 65 70 75 80
 Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr
 85 90 95
 Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile
 100 105 110
 Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn
 115 120 125
 Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile
 130 135 140
 Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys
 145 150 155 160
 Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile
 165 170 175
 Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp
 180 185 190
 Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr
 195 200 205
 Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg
 210 215 220
 Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser
 225 230 235 240
 Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
 245 250 255
 Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr
 260 265 270
 Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn
 275 280 285
 Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile
 290 295 300
 Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
 305 310 315 320
 Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
 325 330 335

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Ser	Tyr	Arg	Val	Tyr	Val	Leu	Val	Asn	Ser	Lys	Glu	Ile	Gln	Thr	Gln	
			340					345					350			
Leu	Phe	Leu	Ala	Pro	Ile	Asn	Asp	Asp	Pro	Thr	Phe	Tyr	Asp	Val	Leu	
		355					360					365				
Gln	Ile	Lys	Lys	Tyr	Tyr	Glu	Lys	Thr	Thr	Tyr	Asn	Cys	Gln	Ile	Leu	
	370					375					380					
Cys	Glu	Lys	Asp	Thr	Lys	Thr	Phe	Gly	Leu	Phe	Gly	Ile	Gly	Lys	Phe	
385					390					395					400	
Val	Lys	Asp	Tyr	Gly	Tyr	Val	Trp	Asp	Thr	Tyr	Asp	Asn	Tyr	Phe	Cys	
				405					410					415		
Ile	Ser	Gln	Trp	Tyr	Leu	Arg	Arg	Ile	Ser	Glu	Asn	Ile	Asn	Lys	Leu	
		420						425					430			
Arg	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	Pro	Val	Asp	Glu	Gly	Trp	Thr	
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Glu																

<210> 19
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
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 <221> CDS
 <222> (1)...(1239)

<400> 19																
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Met	Ala	Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe	
1				5					10					15		
ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa																96
Phe	Ser	Pro		Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	
			20					25					30			
gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct																144
Glu	Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	
			35				40					45				
ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa																192
Leu	Asp	Leu	Ile	Gln	Gln	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu		
			50			55				60						
ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag																240
Pro	Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	
			65			70				75					80	
ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac																288
Leu	Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	
				85				90					95			
gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc																336
Glu	Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	
			100					105					110			
gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct																384
Glu	His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	
			115				120						125			

ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt	432
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val	
130 135 140	
aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt	480
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val	
145 150 155 160	
gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc	528
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr	
165 170 175	
act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg	576
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro	
180 185 190	
gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct	624
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala	
195 200 205	
ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc	672
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile	
210 215 220	
gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac	720
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn	
225 230 235 240	
aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac	768
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn	
245 250 255	
gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct	816
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala	
260 265 270	
aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct	864
Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala	
275 280 285	
ctg gaa aac cag gct gaa gct act aaa gct atc atc aac tac cag tac	912
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr	
290 295 300	
aac cag tac acc gaa gaa gaa aag aac aac atc aac ttc aac atc gat	960
Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp	
305 310 315 320	
gac ctg tcc tct aaa ctg aac gaa tcc atc aac aaa gct atg atc aac	1008
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn	
325 330 335	
atc aac aaa ttc ctg aac cag tgc tct gtt tcc tac ctg atg aac tct	1056
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser	
340 345 350	
atg atc ccg tac ggc gtt aaa cgc ctg gaa gac ttc gac gct tcc ctg	1104
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu	
355 360 365	

	130				135				140								
gtc Val 145	gag Glu	gcc Ala	ggt Gly	ttg Leu	ttc Phe 150	gct Ala	ggt Gly	tgg Trp	gtc Val	aag Lys 155	cag Gln	atc Ile	gtc Val	aac Asn	gat Asp 160	480	
ttc Phe	gtc Val	atc Ile	gag Glu	gct Ala 165	aac Asn	aag Lys	tcc Ser	aac Asn	acc Thr 170	atg Met	gac Asp	aag Lys	att Ile	gcc Ala 175	gac Asp	528	
atc Ile	tcc Ser	ttg Leu	att Ile 180	gtc Val	cca Pro	tac Tyr	atc Ile	ggt Gly 185	ttg Leu	gcc Ala	ttg Leu	aac Asn	gtc Val 190	ggt Gly	aac Asn	576	
gag Glu	acc Thr	gcc Ala 195	aag Lys	ggt Gly	aac Asn	ttc Phe	gag Glu 200	aac Asn	gct Ala	ttc Phe	gag Glu	atc Ile 205	gct Ala	ggt Gly	gcc Ala	624	
tcc Ser 210	atc Ile	ttg Leu	ttg Leu	gag Glu	ttc Phe 215	atc Ile	cca Pro	gag Glu	ttg Leu	ttg Leu	atc Ile 220	cca Pro	gtc Val	gtc Val	ggt Gly	672	
gcc Ala 225	ttc Phe	ttg Leu	ttg Leu	gag Glu	tcc Ser 230	tac Tyr	atc Ile	gac Asp	aac Asn	aag Lys 235	aac Asn	aag Lys	atc Ile	atc Ile	aag Lys 240	720	
acc Thr	atc Ile	gac Asp	aac Asn	gct Ala 245	ttg Leu	acc Thr	aag Lys	aga Arg	aac Asn 250	gag Glu	aag Lys	tgg Trp	tcc Ser	gac Asp 255	atg Met	768	
tac Tyr	ggt Gly	ttg Leu	atc Ile 260	gtc Val	gcc Ala	caa Gln	tgg Trp	ttg Leu	tcc Ser	acc Thr	gtc Val	aac Asn	acc Thr 270	caa Gln	ttc Phe	816	
tac Tyr	acc Thr	atc Ile 275	aag Lys	gag Glu	ggt Gly	atg Met	tac Tyr 280	aag Lys	gcc Ala	ttg Leu	aac Asn	tac Tyr 285	cag Gln	gcc Ala	caa Gln	864	
gct Ala 290	ttg Leu	gag Glu	gag Glu	atc Ile	atc Ile	aag Lys 295	tac Tyr	aga Arg	tac Tyr	aac Asn	atc Ile 300	tac Tyr	tcc Ser	gag Glu	aag Lys	912	
gag Glu 305	aag Lys	tcc Ser	aac Asn	att Ile	aac Asn 310	atc Ile	gac Asp	ttc Phe	aac Asn	gac Asp 315	atc Ile	aac Asn	tcc Ser	aag Lys	ctg Leu 320	960	
aac Asn	gag Glu	ggt Gly	att Ile 325	aac Asn	cag Gln	gcc Ala	atc Ile	gac Asp	aac Asn 330	atc Ile	aac Asn	aac Asn	ttc Phe	atc Ile 335	aac Asn	1008	
ggt Gly	tgt Cys	tcc Ser	gtc Val 340	tcc Ser	tac Tyr	ttg Leu	atg Met	aag Lys 345	aag Lys	atg Met	att Ile	cca Pro	ttg Leu 350	gcc Ala	gtc Val	1056	
gag Glu	aag Lys	ttg Leu 355	ttg Leu	gac Asp	ttc Phe	gac Asp 360	aac Asn	acc Thr	ctg Leu	aag Lys	aag Lys	aac Asn 365	ttg Leu	ttg Leu	aac Asn	1104	
tac Tyr	atc Ile 370	gac Asp	gag Glu	aac Asn	aag Lys 375	ttg Leu	tac Tyr	ttg Leu	atc Ile	ggt Gly 380	tcc Ser	gct Ala	gag Glu	tac Tyr	gag Glu	1152	

Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val	
			340					345					350			
Glu	Lys	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn		
		355				360					365					
Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu	
	370					375					380					
Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu	
385				390						395					400	
Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe				
			405					410								

<210> 23
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 <212> DNA
 <213> Artificial Sequence

<220>
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<221> CDS
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Met	Ser	Leu	Tyr	Asn	Lys	Thr	Leu	Asp	Cys	Arg	Glu	Leu	Leu	Val	Lys	
1				5				10				15				
aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac																96
Asn	Thr	Asp	Leu	Pro	Phe	Ile	Gly	Asp	Ile	Ser	Asp	Val	Lys	Thr	Asp	
		20					25					30				
atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac																144
Ile	Phe	Leu	Arg	Lys	Asp	Ile	Asn	Glu	Glu	Thr	Glu	Val	Ile	Tyr	Tyr	
		35				40					45					
cca gac aac gtg tca gta gac caa gtg atc ctc agt aag aac acc tcc																192
Pro	Asp	Asn	Val	Ser	Val	Asp	Gln	Val	Ile	Leu	Ser	Lys	Asn	Thr	Ser	
	50					55				60						
gag cat gga caa cta gac ctg ctc tac cct agt atc gac agt gag agt																240
Glu	His	Gly	Gln	Leu	Asp	Leu	Leu	Tyr	Pro	Ser	Ile	Asp	Ser	Glu	Ser	
65				70				75					80			
gag atc ctg cca ggg gag aat caa gtc ttc tac gac aac cgt acc cag																288
Glu	Ile	Leu	Pro	Gly	Glu	Asn	Gln	Val	Phe	Tyr	Asp	Asn	Arg	Thr	Gln	
			85				90						95			
aac gtg gac tac ctg aac tcc tac tac tac cta gag tct cag aag ctg																336
Asn	Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu	
			100				105						110			
agt gac aac gtg gag gac ttc act ttc acg cgt tca atc gag gag gct																384
Ser	Asp	Asn	Val	Glu	Asp	Phe	Thr	Phe	Thr	Arg	Ser	Ile	Glu	Glu	Ala	
	115					120						125				
ctg gac aac agt gca aag gtg tac act tac ttc cct acc ctg gct aac																432
Leu	Asp	Asn	Ser	Ala	Lys	Val	Tyr	Thr	Tyr	Phe	Pro	Thr	Leu	Ala	Asn	
	130					135					140					
aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac																480

Lys 145	Val	Asn	Ala	Gly	Val 150	Gln	Gly	Gly	Leu	Phe 155	Leu	Met	Trp	Ala	Asn 160		
gac Asp	gtg Val	gtt Val	gag Glu	gac Asp 165	ttc Phe	act Thr	acc Thr	aac Asn	atc Ile 170	ctg Leu	cgt Arg	aag Lys	gac Asp	aca Thr 175	ctg Leu	528	
gac Asp	aag Lys	atc Ile 180	tca Ser	gat Asp	gtg Val	tca Ser	gct Ala	atc Ile 185	atc Ile	ccc Pro	tac Tyr	atc Ile	gga Gly 190	ccc Pro	gca Ala	576	
ctg Leu	aac Asn 195	atc Ile	tcc Ser	aac Asn	tct Ser	gtg Val	cgt Arg 200	cgt Arg	gga Gly	aac Asn	ttc Phe 205	act Thr	gag Glu	gca Ala	ttc Phe	624	
gca Ala 210	gtc Val	act Thr	ggg Gly	gtc Val	acc Thr	atc Ile 215	ctg Leu	ctg Leu	gag Glu	gca Ala	ttc Phe 220	cct Pro	gag Glu	ttc Phe	aca Thr	672	
atc Ile 225	cct Pro	gct Ala	ctg Leu	ggg Gly	gca Ala 230	ttc Phe	gtg Val	atc Ile	tac Tyr	agt Ser 235	aag Lys	gtc Val	cag Gln	gag Glu	cga Arg 240	720	
aac Asn	gag Glu	atc Ile	atc Ile	aag Lys 245	acc Thr	atc Ile	gac Asp	aac Asn	tgt Cys 250	ctg Leu	gag Glu	cag Gln	agg Arg	atc Ile 255	aag Lys	768	
aga Arg	tgg Trp	aag Lys 260	gac Asp	tcc Ser	tac Tyr	gag Glu	tgg Trp	atg Met 265	atg Met	gga Gly	acg Thr	tgg Trp	ttg Leu 270	tcc Ser	agg Arg	816	
atc Ile	atc Ile	acc Thr 275	cag Gln	ttc Phe	aac Asn	aac Asn	atc Ile 280	tcc Ser	tac Tyr	cag Gln	atg Met 285	tac Tyr	gac Asp	tcc Ser	ctg Leu	864	
aac Asn 290	tac Tyr	cag Gln	gca Ala	ggg Gly	gca Ala 295	atc Ile	aag Lys	gct Ala	aag Lys	atc Ile	gac Asp 300	ctg Leu	gag Glu	tac Tyr	aag Lys	912	
aag Lys 305	tac Tyr	tcc Ser	gga Gly	agc Ser	gac Asp 310	aag Lys	gag Glu	aac Asn	atc Ile	aag Lys 315	agc Ser	cag Gln	gtt Val	gag Glu	aac Asn 320	960	
ctg Leu	aag Lys	aac Asn	agt Ser 325	ctg Leu	gac Asp	gtc Val	aag Lys	atc Ile	tcc Ser 330	gag Glu	gca Ala	atg Met	aac Asn	aac Asn	atc Ile 335	1008	
aac Asn	aag Lys	ttc Phe 340	atc Ile	cga Arg	gag Glu	tgc Cys	tcc Ser	gtc Val 345	acc Thr	tac Tyr	ctg Leu	ttc Phe	aag Lys 350	aac Asn	atg Met	1056	
ctg Leu	cct Pro 355	aag Lys	gtc Val	atc Ile	gac Asp	gag Glu	ctg Leu 360	aac Asn	gag Glu	ttc Phe	gac Asp	cga Arg	aac Asn	acc Thr	aag Lys	1104	
gca Ala 370	aag Lys	ctg Leu	atc Ile	aac Asn	ctg Leu	atc Ile 375	gac Asp	tcc Ser	cat His	aac Asn	atc Ile 380	atc Ile	ctg Leu	gtc Val	ggg Gly	1152	
gag Glu	gtc Val	gac Asp	aag Lys	ctg Leu	aag Lys	gca Ala	aag Lys	gta Val	aac Asn	aac Asn	agc Ser	ttc Phe	cag Gln	aac Asn		1197	

385

390

395

taa

1200

<210> 24

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

Met	Ser	Leu	Tyr	Asn	Lys	Thr	Leu	Asp	Cys	Arg	Glu	Leu	Leu	Val	Lys
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Asn	Thr	Asp	Leu	Pro	Phe	Ile	Gly	Asp	Ile	Ser	Asp	Val	Lys	Thr	Asp
		20					25					30			
Ile	Phe	Leu	Arg	Lys	Asp	Ile	Asn	Glu	Glu	Thr	Glu	Val	Ile	Tyr	Tyr
	35					40					45				
Pro	Asp	Asn	Val	Ser	Val	Asp	Gln	Val	Ile	Leu	Ser	Lys	Asn	Thr	Ser
	50				55					60					
Glu	His	Gly	Gln	Leu	Asp	Leu	Leu	Tyr	Pro	Ser	Ile	Asp	Ser	Glu	Ser
65				70					75					80	
Glu	Ile	Leu	Pro	Gly	Glu	Asn	Gln	Val	Phe	Tyr	Asp	Asn	Arg	Thr	Gln
			85						90				95		
Asn	Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu
		100					105					110			
Ser	Asp	Asn	Val	Glu	Asp	Phe	Thr	Phe	Thr	Arg	Ser	Ile	Glu	Glu	Ala
	115						120					125			
Leu	Asp	Asn	Ser	Ala	Lys	Val	Tyr	Thr	Tyr	Phe	Pro	Thr	Leu	Ala	Asn
	130				135					140					
Lys	Val	Asn	Ala	Gly	Val	Gln	Gly	Gly	Leu	Phe	Leu	Met	Trp	Ala	Asn
145				150					155					160	
Asp	Val	Val	Glu	Asp	Phe	Thr	Thr	Asn	Ile	Leu	Arg	Lys	Asp	Thr	Leu
			165					170					175		
Asp	Lys	Ile	Ser	Asp	Val	Ser	Ala	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala
	180						185					190			
Leu	Asn	Ile	Ser	Asn	Ser	Val	Arg	Arg	Gly	Asn	Phe	Thr	Glu	Ala	Phe
	195					200					205				
Ala	Val	Thr	Gly	Val	Thr	Ile	Leu	Leu	Glu	Ala	Phe	Pro	Glu	Phe	Thr
	210				215					220					
Ile	Pro	Ala	Leu	Gly	Ala	Phe	Val	Ile	Tyr	Ser	Lys	Val	Gln	Glu	Arg
225				230					235					240	
Asn	Glu	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Lys
			245					250					255		
Arg	Trp	Lys	Asp	Ser	Tyr	Glu	Trp	Met	Met	Gly	Thr	Trp	Leu	Ser	Arg
		260					265					270			
Ile	Ile	Thr	Gln	Phe	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Tyr	Asp	Ser	Leu
	275					280					285				
Asn	Tyr	Gln	Ala	Gly	Ala	Ile	Lys	Ala	Lys	Ile	Asp	Leu	Glu	Tyr	Lys
	290				295				300						
Lys	Tyr	Ser	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Lys	Ser	Gln	Val	Glu	Asn
305				310					315					320	
Leu	Lys	Asn	Ser	Leu	Asp	Val	Lys	Ile	Ser	Glu	Ala	Met	Asn	Asn	Ile
			325					330					335		
Asn	Lys	Phe	Ile	Arg	Glu	Cys	Ser	Val	Thr	Tyr	Leu	Phe	Lys	Asn	Met
	340						345					350			
Leu	Pro	Lys	Val	Ile	Asp	Glu	Leu	Asn	Glu	Phe	Asp	Arg	Asn	Thr	Lys
	355					360					365				
Ala	Lys	Leu	Ile	Asn	Leu	Ile	Asp	Ser	His	Asn	Ile	Ile	Leu	Val	Gly
	370				375						380				

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Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
 385 390 395

<210> 25
 <211> 1161
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1158)

<400> 25
 atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac 48
 Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1 5 10 15

aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc 96
 Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
 20 25 30

gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac 144
 Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
 35 40 45

aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac 192
 Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
 50 55 60

cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg 240
 Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
 65 70 75 80

aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac 288
 Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
 85 90 95

gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct 336
 Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
 100 105 110

aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg 384
 Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
 115 120 125

ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag 432
 Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
 130 135 140

gtt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag 480
 Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
 145 150 155 160

gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac 528
 Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
 165 170 175

aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg 576

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[illegible]

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<210> 26
<211> 386
<212> PRT
<213> Artificial Sequence
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<220>

<223> Synthetic Construct

<400> 26

Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
1 5 10 15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
20 25 30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
35 40 45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
50 55 60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65 70 75 80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
85 90 95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
100 105 110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Ala Leu
115 120 125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
130 135 140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145 150 155 160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
165 170 175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
180 185 190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
195 200 205
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
210 215 220
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225 230 235 240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
245 250 255
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
260 265 270
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
275 280 285
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
290 295 300
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305 310 315 320
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
325 330 335
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
340 345 350
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
355 360 365
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
370 375 380
Val Asp
385

<210> 27

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<221> CDS

<222> (1)...(1146)

<400> 27

atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct	48
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala	
1 5 10 15	
tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att	96
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile	
20 25 30	
gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag	144
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln	
35 40 45	
gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag	192
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu	
50 55 60	
aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac	240
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp	
65 70 75 80	
tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac	288
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn	
85 90 95	
gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac	336
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn	
100 105 110	
gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag	384
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys	
115 120 125	
atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct	432
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro	
130 135 140	
gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac	480
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp	
145 150 155 160	
ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac	528
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp	
165 170 175	
atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac	576
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn	
180 185 190	
gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc	624
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala	
195 200 205	
ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg	672
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu	

210	215	220	
gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag			720
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys			
225	230	235	240
gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg			768
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp			
	245	250	255
aag gaa gtc tat tcc ttc atc gtc tct aac tgg atg acc aag atc aac			816
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn			
	260	265	270
acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac			864
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn			
	275	280	285
cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac			912
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr			
	290	295	300
acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag			960
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln			
305	310	315	320
atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc			1008
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile			
	325	330	335
gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc			1056
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile			
	340	345	350
aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag			1104
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys			
	355	360	365
acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg			1146
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu			
	370	375	380
taa			1149
<210> 28			
<211> 382			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Synthetic Construct			
<400> 28			
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala			
1 5 10 15			
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile			
20 25 30			
Asp Asp Thr Val Thr Ser Asn Asn Tyr Glu Asn Asp Leu Asp Gln			
35 40 45			
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu			
50 55 60			


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att aac act caa ttt aac aag aga aag gag caa atg tac cag gct ctg 864
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
      275                      280                      285

caa aac caa gtc gat gct atc aag act gca att gaa tac aag tac aac 912
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
      290                      295                      300

aac tat act tcc gat gag aag aac aga ctt gaa tct gaa tac aat atc 960
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
      305                      310                      315

aac aac att gaa gaa gag ttg aac aag aaa gtt tct ttg gct atg aag 1008
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
      325                      330                      335

aat atc gaa aga ttt atg acc gaa tcc tct atc tct tac ttg atg aag 1056
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
      340                      345                      350

ttg atc aat gag gcc aag gtt ggt aag ttg aag aag tac gat aac cac 1104
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
      355                      360                      365

gtt aag agc gat ctg ctg aac tac att ctc gac cac aga tca atc ctg 1152
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
      370                      375                      380

gga gag cag aca aac gag ctg agt gat ttg gtt act tcc act ttg aac 1200
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
      385                      390                      395                      400

tcc tcc att cca ttt gag ctt tct taa 1227
Ser Ser Ile Pro Phe Glu Leu Ser
      405

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<210> 30
 <211> 408
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<400> 30
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1      5      10      15
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
      20      25      30
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
      35      40      45
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
      50      55      60
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
      65      70      75      80
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
      85      90      95
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
      100      105      110
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu

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tta aat aat caa tca caa gca ata gaa aaa ata ata gaa gat caa tat	912
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr	
290 295 300	
aat aga tat agt gaa gaa gat aaa atg aat att aac att gat ttt aat	960
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn	
305 310 315 320	
gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat	1008
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn	
325 330 335	
ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga	1056
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg	
340 345 350	
atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt	1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu	
355 360 365	
aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt	1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu	
370 375 380	
gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac	1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp	
385 390 395 400	
agt ata cca ttt gat ctt tca cta tat acc taa	1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr	
405 410	

<210> 32
 <211> 410
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
1 5 10 15
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
20 25 30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
35 40 45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
50 55 60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65 70 75 80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
85 90 95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
100 105 110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
115 120 125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
130 135 140

Glu	Lys	Ala	Asn	Thr	Val	Val	Gly	Ala	Ser	Leu	Phe	Val	Asn	Trp	Val	145	150	155	160
Lys	Gly	Val	Ile	Asp	Asp	Phe	Thr	Ser	Glu	Ser	Thr	Gln	Lys	Ser	Thr	165	170	175	
Ile	Asp	Lys	Val	Ser	Asp	Val	Ser	Ile	Ile	Pro	Tyr	Ile	Gly	Pro		180	185	190	
Ala	Leu	Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Glu	Asn	Phe	Lys	Asn	Ala	195	200	205	
Phe	Glu	Ile	Gly	Gly	Ala	Ala	Ile	Leu	Met	Glu	Phe	Ile	Pro	Glu	Leu	210	215	220	
Ile	Val	Pro	Ile	Val	Gly	Phe	Phe	Thr	Leu	Glu	Ser	Tyr	Val	Gly	Asn	225	230	235	240
Lys	Gly	His	Ile	Ile	Met	Thr	Ile	Ser	Asn	Ala	Leu	Lys	Lys	Arg	Asp	245	250	255	
Gln	Lys	Trp	Thr	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ser	Gln	Trp	Leu	Ser	260	265	270	
Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Arg	Met	Tyr	Asn	Ala	275	280	285	
Leu	Asn	Asn	Gln	Ser	Gln	Ala	Ile	Glu	Lys	Ile	Ile	Glu	Asp	Gln	Tyr	290	295	300	
Asn	Arg	Tyr	Ser	Glu	Glu	Asp	Lys	Met	Asn	Ile	Asn	Ile	Asp	Phe	Asn	305	310	315	320
Asp	Ile	Asp	Phe	Lys	Leu	Asn	Gln	Ser	Ile	Asn	Leu	Ala	Ile	Asn	Asn	325	330	335	
Ile	Asp	Asp	Phe	Ile	Asn	Gln	Cys	Ser	Ile	Ser	Tyr	Leu	Met	Asn	Arg	340	345	350	
Met	Ile	Pro	Leu	Ala	Val	Lys	Lys	Leu	Lys	Asp	Phe	Asp	Asp	Asn	Leu	355	360	365	
Lys	Arg	Asp	Leu	Leu	Glu	Tyr	Ile	Asp	Thr	Asn	Glu	Leu	Tyr	Leu	Leu	370	375	380	
Asp	Glu	Val	Asn	Ile	Leu	Lys	Ser	Lys	Val	Asn	Arg	His	Leu	Lys	Asp	385	390	395	400
Ser	Ile	Pro	Phe	Asp	Leu	Ser	Leu	Tyr	Thr							405	410		

<210> 33
 <211> 1314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (10)...(1305)

<400> 33
 gaattcagc atg tct tac act aac gac aaa atc ctg atc ctg tac ttc aac 51
 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
 1 10

aaa ctg tac aaa aaa atc aaa gac aac tct atc ctg gac atg cgt tac 99
 Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15 20 25 30

gaa aac aac aaa ttc atc gac atc tct ggc tat ggt tct aac atc tct 147
 Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
 35 40 45

atc aac ggt gac gtc tac atc tac tct act aac cgc aac cag ttc ggt 195

Ile	Asn	Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly		
			50					55					60				
atc	tac	tct	tct	aaa	ccg	tct	gaa	gta	aac	atc	gct	cag	aac	aac	gac	243	
Ile	Tyr	Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp		
		65					70				75						
atc	atc	tac	aac	ggc	cgt	tac	cag	aac	ttc	tct	atc	tct	ttc	tggt	gtt	291	
Ile	Ile	Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val		
	80					85					90						
cgt	atc	ccg	aaa	tac	ttc	aac	aaa	gtt	aac	ctg	aac	aac	gaa	tac	act	339	
Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr		
	95				100					105					110		
atc	atc	gac	tcg	atc	cgt	aac	aac	aac	tct	ggc	tcg	aaa	atc	tct	ctg	387	
Ile	Ile	Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu		
				115					120					125			
aac	tac	aac	aaa	atc	atc	tcg	act	ctg	cag	gac	act	gct	ggc	aac	aac	435	
Asn	Tyr	Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn		
			130					135					140				
cag	aaa	ctg	gtt	ttc	aac	tac	act	cag	atg	atc	tct	atc	tct	gac	tac	483	
Gln	Lys	Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr		
		145					150					155					
att	aac	aaa	tcg	atc	ttc	gtt	act	atc	act	aac	aac	cgt	ctg	ggc	aac	531	
Ile	Asn	Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn		
	160					165					170						
tct	cgt	atc	tac	atc	aac	ggc	aac	ctg	atc	gat	gaa	aaa	tct	atc	tct	579	
Ser	Arg	Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser		
	175				180					185					190		
aac	ctg	ggc	gac	atc	cac	gtt	tct	gac	aac	atc	ctg	ttc	aaa	atc	gtt	627	
Asn	Leu	Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val		
				195					200					205			
ggc	tcg	aac	gac	acg	cgt	tac	gtt	ggc	atc	cgt	tac	ttc	aaa	gtt	ttc	675	
Gly	Cys	Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe		
			210				215						220				
gac	act	gaa	ctg	ggc	aaa	act	gaa	atc	gaa	act	ctg	tac	tct	gac	gaa	723	
Asp	Thr	Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu		
		225					230					235					
ccg	gac	ccg	tct	atc	ctg	aaa	gac	ttc	tcg	ggc	aac	tac	ctg	ctg	tac	771	
Pro	Asp	Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr		
		240				245					250						
aac	aaa	cgt	tac	tac	ctg	ctg	aac	ctg	ctc	cgg	act	gac	aaa	tct	atc	819	
Asn	Lys	Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile		
	255				260					265					270		
act	cag	aac	tct	aac	ttc	ctg	aac	atc	aac	cag	cag	cgt	ggc	gtt	tac	867	
Thr	Gln	Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr		
				275				280						285			
cag	aaa	cct	aac	atc	ttc	tct	aac	act	cgt	ctg	tac	act	ggc	gtt	gaa	915	
Gln	Lys	Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu		

Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr
	115						120					125			
Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys
	130					135					140				
Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn
145					150					155					160
Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg
			165						170					175	
Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu
		180						185					190		
Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys
	195						200					205			
Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr
	210					215					220				
Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp
225					230					235					240
Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys
			245					250						255	
Arg	Tyr	Tyr	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln	
		260					265						270		
Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys
	275						280					285			
Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile
	290					295					300				
Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val
305				310					315					320	
Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu
			325					330					335		
Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile
		340					345						350		
Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile
	355					360						365			
Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn
	370					375					380				
Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	Leu	Val
385					390				395						400
Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser	Ser	Asn
			405					410					415		
Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln	Glu	Asn
			420					425					430		